SEQUENCE LISTING

<110> YAMAKI, TOSHIFUMI
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<140> 10/539,560
<141> 2005-06-16

<150> PCT/JP03/016014
<151> 2003-12-15

<150> JP 2003-379280
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<170> PatentIn Ver. 3.3

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Lys	Glu	Leu	Gly	Ile	Gly	Gly	Leu	Gln	Gly	Glu	Asp	Met	Met	Trp	Val
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Glu Glu Phe Gly Phe Glu Val Pro Pro Ser Lys Glu Ile Lys Val Trp
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Asp Ser Ser Ser Glu Met Arg Phe Val Val Leu Pro Gln Arg Pro Ala
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Val Arg Thr Gly Lys Ile Asp Leu Glu Glu Leu Glu Arg Arg Thr Gln
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Tyr Tyr Arg Glu Asn Pro Asp Ala Pro Leu Pro Glu His Glu Gln Lys
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Pro Glu Leu Ile Glu Phe Val Asn Gln Ala Val Tyr Gly Gly Leu Pro
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Asp Leu Asp Asp Pro Ser Trp Ser Tyr Tyr Glu His Phe Val Ala Ala
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<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 92
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<210> 93
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<400> 93
aacggccggg gcgagtgc 18

<210> 94
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<400> 94
aacggcaacg gcgagtgc 18

<210> 95
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<400> 95
aacggctcgg gcgagtgc 18

<210> 96
<211> 18
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<220>
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<400> 96
aacggcgggg gcgagtgc 18

<210> 97
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<400> 97
tactacggct gctgggag 18

<210> 98
<211> 205
<212> PRT
<213> Pseudonocardia thermophila

<400> 98

Met	Thr	Glu	Asn	Ile	Leu	Arg	Lys	Ser	Asp	Glu	Glu	Ile	Gln	Lys	Glu
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Ile	Thr	Ala	Arg	Val	Lys	Ala	Leu	Glu	Ser	Met	Leu	Ile	Glu	Gln	Gly
			20					25					30		
Ile	Leu	Thr	Thr	Ser	Met	Ile	Asp	Arg	Met	Ala	Glu	Ile	Tyr	Glu	Asn
		35					40					45			
Glu	Val	Gly	Pro	His	Leu	Gly	Ala	Lys	Val	Val	Val	Lys	Ala	Trp	Thr
	50					55					60				
Asp	Pro	Glu	Phe	Lys	Lys	Arg	Leu	Leu	Ala	Asp	Gly	Thr	Glu	Ala	Cys
65					70					75					80
Lys	Glu	Leu	Gly	Ile	Gly	Gly	Leu	Gln	Gly	Glu	Asp	Met	Met	Trp	Val
				85					90					95	
Glu	Asn	Thr	Asp	Glu	Val	His	His	Val	Val	Val	Cys	Thr	Leu	Cys	Ser
			100					105					110		

Cys Tyr Pro Trp Pro Val Leu Gly Leu Pro Pro Asn Trp Phe Lys Glu
115 120 125

Pro Gln Tyr Arg Ser Arg Val Val Arg Glu Pro Arg Gln Leu Leu Lys
130 135 140

Glu Glu Phe Gly Phe Glu Val Pro Pro Ser Lys Glu Ile Lys Val Trp
145 150 155 160

Asp Ser Ser Ser Glu Met Arg Phe Val Val Leu Pro Gln Arg Pro Ala
165 170 175

Gly Thr Asp Gly Trp Ser Glu Glu Glu Leu Ala Thr Leu Val Thr Arg
180 185 190

Glu Ser Met Ile Gly Val Glu Pro Ala Lys Ala Val Ala
195 200 205

<210> 99
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<212> PRT
<213> Pseudonocardia thermophila

<400> 99
Met Asn Gly Val Tyr Asp Val Gly Gly Thr Asp Gly Leu Gly Pro Ile
1 5 10 15

Asn Arg Pro Ala Asp Glu Pro Val Phe Arg Ala Glu Trp Glu Lys Val
20 25 30

Ala Phe Ala Met Phe Pro Ala Thr Phe Arg Ala Gly Phe Met Gly Leu
35 40 45

Asp Glu Phe Arg Phe Gly Ile Glu Gln Met Asn Pro Ala Glu Tyr Leu
50 55 60

Glu Ser Pro Tyr Tyr Trp His Trp Ile Arg Thr Tyr Ile His His Gly
65 70 75 80

Val Arg Thr Gly Lys Ile Asp Leu Glu Glu Leu Glu Arg Arg Thr Gln
85 90 95

Tyr Tyr Arg Glu Asn Pro Asp Ala Pro Leu Pro Glu His Glu Gln Lys
100 105 110

Pro Glu Leu Ile Glu Phe Val Asn Gln Ala Val Tyr Gly Gly Leu Pro
115 120 125

Ala Ser Arg Glu Val Asp Arg Pro Pro Lys Phe Lys Glu Gly Asp Val
130 135 140

Val Arg Phe Ser Thr Ala Ser Pro Lys Gly His Ala Arg Arg Ala Arg
145 150 155 160

Tyr Val Arg Gly Lys Thr Gly Thr Val Val Lys His His Gly Ala Tyr
165 170 175

Ile Tyr Pro Asp Thr Ala Gly Asn Gly Leu Gly Glu Cys Pro Glu His
180 185 190

Leu Tyr Thr Val Arg Phe Thr Ala Gln Glu Leu Trp Gly Pro Glu Gly
195 200 205

Asp Pro Asn Ser Ser Val Tyr Tyr Asp Cys Trp Glu Pro Tyr Ile Glu
210 215 220

Leu Val Asp Thr Lys Ala Ala Ala Ala
225 230

<210> 100
<211> 618
<212> DNA
<213> Pseudonocardia thermophila

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gtcaaggccc tggagtcgat gctcatcgaa cagggcatcc tcaccacgtc gatgatcgac 120
cggatggccg agatctacga gaacgaggtc ggcccgcacc tcggcgcgaa ggtcgtcgtg 180
aaggcctgga ccgacccgga gttcaagaag cgtctgctcg ccgacggcac cgaggcctgc 240
aaggagctcg gcatcggcgg cctgcagggc gaggacatga tgtgggtgga gaacaccgac 300
gaggtccacc acgtcgtcgt gtgcacgctc tgctcctgct acccgtggcc ggtgctgggg 360
ctgccgccga actggttcaa ggagccgcag taccgctccc gcgtggtgcg tgagccccgg 420
cagctgctca aggaggagtt cggcttcgag gtcccgccga gcaaggagat caaggtctgg 480
gactccagct ccgagatgcg cttcgtcgtc ctcccgcagc gccccgcggg caccgacggg 540
tggagcgagg aggagctcgc caccctcgtc acccgcgagt cgatgatcgg cgtcgaaccg 600
gcgaaggcgg tcgcgtga 618

<210> 101
<211> 702
<212> DNA
<213> Pseudonocardia thermophila

<400> 101
atgaacggcg tgtacgacgt cggcggcacc gatgggctgg gcccgatcaa ccggcccgcg 60
gacgaaccgg tcttccgcgc cgagtgggag aaggtcgcgt tcgcgatgtt cccggcgacg 120
ttccgggccg gcttcatggg cctggacgag ttccggttcg gcatcgagca gatgaacccg 180
gccgagtacc tcgagtcgcc gtactactgg cactggatcc gcacctacat ccaccacggc 240
gtccgcaccg gcaagatcga tctcgaggag ctggagcgcc gcacgcagta ctaccgggag 300
aaccccgacg ccccgctgcc cgagcacgag cagaagccgg agttgatcga gttcgtcaac 360
caggccgtct acggcgggct gcccgcaagc cgggaggtcg accgaccgcc caagttcaag 420
gagggcgacg tggtgcggtt ctccaccgcg agcccgaagg gccacgcccg gcgcgcgcgg 480
tacgtgcgcg gcaagaccgg gacggtggtc aagcaccacg gcgcgtacat ctacccggac 540
accgccggca acggcctggg cgagtgcccc gagcacctct acaccgtccg cttcacggcc 600
caggagctgt gggggccgga aggggacccg aactccagcg tctactacga ctgctgggag 660
ccctacatcg agctcgtcga cacgaaggcg gccgcggcat ga 702

<210> 102
<211> 144
<212> PRT
<213> Pseudonocardia thermophila

<400> 102
Met Ser Ala Glu Ala Lys Val Arg Leu Lys His Cys Pro Thr Ala Glu
1 5 10 15

Asp Arg Ala Ala Ala Asp Ala Leu Leu Ala Gln Leu Pro Gly Gly Asp
20 25 30

Arg Ala Leu Asp Arg Gly Phe Asp Glu Pro Trp Gln Leu Arg Ala Phe
35 40 45

Ala Leu Ala Val Ala Ala Cys Arg Ala Gly Arg Phe Glu Trp Lys Gln
50 55 60

Leu Gln Gln Ala Leu Ile Ser Ser Ile Gly Glu Trp Glu Arg Thr His
65 70 75 80

Asp Leu Asp Asp Pro Ser Trp Ser Tyr Tyr Glu His Phe Val Ala Ala
85 90 95

Leu Glu Ser Val Leu Gly Glu Glu Gly Ile Val Glu Pro Glu Ala Leu
100 105 110

Asp Glu Arg Thr Ala Glu Val Leu Ala Asn Pro Pro Asn Lys Asp His
115 120 125

His Gly Pro His Leu Glu Pro Val Ala Val His Pro Ala Val Arg Ser
130 135 140

<210> 103
<211> 435
<212> DNA
<213> Pseudonocardia thermophila

<400> 103
rtgagcgccg aggcgaaggt ccgcctgaag cactgcccca cggccgagga ccgggcggcg 60
gccgacgcgc tgctcgcgca gctgcccggc ggcgaccgcg cgctcgaccg cggcttcgac 120
gagccgtggc agctgcgggc gttcgcgctg gcggtcgcgg cgtgcagggc gggccggttc 180
gagtggaagc agctgcagca ggcgctgatc tcctcgatcg gggagtggga gcgcacccac 240
gatctcgacg atccgagctg gtcctactac gagcacttcg tcgccgcgct ggaatccgtg 300
ctcggcgagg aagggatcgt cgagccggag gcgctggacg agcgcaccgc ggaggtcttg 360
gccaacccgc cgaacaagga tcaccatgga ccgcatctgg agcccgtcgc ggtccacccg 420
gccgtgcggt cctga 435

<210> 104
<211> 1315
<212> DNA
<213> Rhodococcus rhodochrous

<220>
<221> CDS
<222> (1)..(690)

<220>
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<400> 104

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atg gat ggt atc cac gac aca ggc ggc atg acc gga tac gga ccg gtc    48
Met Asp Gly Ile His Asp Thr Gly Gly Met Thr Gly Tyr Gly Pro Val
  1               5                  10                  15

ccc tat cag aag gac gag ccc ttc ttc cac tac gag tgg gag ggt cgg    96
Pro Tyr Gln Lys Asp Glu Pro Phe Phe His Tyr Glu Trp Glu Gly Arg
             20                  25                  30

acc ctg tca att ctg act tgg atg cat ctc aag ggc ata tcg tgg tgg   144
Thr Leu Ser Ile Leu Thr Trp Met His Leu Lys Gly Ile Ser Trp Trp
         35                  40                  45

gac aag tcg cgg ttc ttc cgg gag tcg atg ggg aac gaa aac tac gtc   192
Asp Lys Ser Arg Phe Phe Arg Glu Ser Met Gly Asn Glu Asn Tyr Val
     50                  55                  60

aac gag att cgc aac tcg tac tac acc cac tgg ctg agt gcg gca gaa   240
Asn Glu Ile Arg Asn Ser Tyr Tyr Thr His Trp Leu Ser Ala Ala Glu
 65                  70                  75                  80

cgt atc ctc gtc gcc gac aag atc atc acc gaa gaa gag cga aag cac   288
Arg Ile Leu Val Ala Asp Lys Ile Ile Thr Glu Glu Glu Arg Lys His
                 85                  90                  95

cgt gtg caa gag atc ctt gag ggt cgg tac acg gac agg aag ccg tcg   336
Arg Val Gln Glu Ile Leu Glu Gly Arg Tyr Thr Asp Arg Lys Pro Ser
            100                 105                 110

cgg aag ttc gat ccg gcc cag atc gag aag gcg atc gaa cgg ctt cac   384
Arg Lys Phe Asp Pro Ala Gln Ile Glu Lys Ala Ile Glu Arg Leu His
        115                 120                 125

gag ccc cac tcc cta gcg ctt cca gga gcg gag ccg agt ttc tct ctc   432
Glu Pro His Ser Leu Ala Leu Pro Gly Ala Glu Pro Ser Phe Ser Leu
    130                 135                 140

ggt gac aag atc aaa gtg aag agt atg aac ccg ctg gga cac aca cgg   480
Gly Asp Lys Ile Lys Val Lys Ser Met Asn Pro Leu Gly His Thr Arg
145                 150                 155                 160

tgc ccg aaa tat gtg cgg aac aag atc ggg gaa atc gtc gcc tac cac   528
Cys Pro Lys Tyr Val Arg Asn Lys Ile Gly Glu Ile Val Ala Tyr His
                165                 170                 175

ggc tgc cag atc tat ccc gag agc agc tcc gcc ggc ctc ggc gac gat   576
Gly Cys Gln Ile Tyr Pro Glu Ser Ser Ser Ala Gly Leu Gly Asp Asp
            180                 185                 190

cct cgc ccg ctc tac acg gtc gcg ttt tcc gcc cag gaa ctg tgg ggc   624
Pro Arg Pro Leu Tyr Thr Val Ala Phe Ser Ala Gln Glu Leu Trp Gly
        195                 200                 205
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gac gac gga aac ggg aaa gac gta gtg tgc gtc gat ctc tgg gaa ccg   672
Asp Asp Gly Asn Gly Lys Asp Val Val Cys Val Asp Leu Trp Glu Pro
    210                 215                 220

tac ctg atc tct gcg tgaaaggaat acgata gtg agc gag cac gtc aat aag 724
Tyr Leu Ile Ser Ala                   Met Ser Glu His Val Asn Lys
225                                     1               5

tac acg gag tac gag gca cgt acc aag gcg atc gaa acc ttg ctg tac   772
Tyr Thr Glu Tyr Glu Ala Arg Thr Lys Ala Ile Glu Thr Leu Leu Tyr
         10                  15                  20

gag cga ggg ctc atc acg ccc gcc gcg gtc gac cga gtc gtt tcg tac   820
Glu Arg Gly Leu Ile Thr Pro Ala Ala Val Asp Arg Val Val Ser Tyr
     25                  30                  35

tac gag aac gag atc ggc ccg atg ggc ggt gcc aag gtc gtg gcc aag   868
Tyr Glu Asn Glu Ile Gly Pro Met Gly Gly Ala Lys Val Val Ala Lys
 40                  45                  50                  55

tcc tgg gtg gac cct gag tac cgc aag tgg ctc gaa gag gac gcg acg   916
Ser Trp Val Asp Pro Glu Tyr Arg Lys Trp Leu Glu Glu Asp Ala Thr
                 60                  65                  70

gcc gcg atg gcg tca ttg ggc tat gcc ggt gag cag gca cac caa att   964
Ala Ala Met Ala Ser Leu Gly Tyr Ala Gly Glu Gln Ala His Gln Ile
             75                  80                  85

tcg gcg gtc ttc aac gac tcc caa acg cat cac gtg gtg gtg tgc act   1012
Ser Ala Val Phe Asn Asp Ser Gln Thr His His Val Val Val Cys Thr
         90                  95                  100

ctg tgt tcg tgc tat ccg tgg ccg gtg ctt ggt ctc ccg ccc gcc tgg   1060
Leu Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly Leu Pro Pro Ala Trp
    105                 110                 115

tac aag agc atg gag tac cgg tcc cga gtg gta gcg gac cct cgt gga   1108
Tyr Lys Ser Met Glu Tyr Arg Ser Arg Val Val Ala Asp Pro Arg Gly
120                 125                 130                 135

gtg ctc aag cgc gat ttc ggt ttc gac atc ccc gat gag gtg gag gtc   1156
Val Leu Lys Arg Asp Phe Gly Phe Asp Ile Pro Asp Glu Val Glu Val
                140                 145                 150

agg gtt tgg gac agc agc tcc gaa atc cgc tac atc gtc atc ccg gaa   1204
Arg Val Trp Asp Ser Ser Ser Glu Ile Arg Tyr Ile Val Ile Pro Glu
            155                 160                 165

cgg ccg gcc ggc acc gac ggt tgg tcc gag gag gag ctg acg aag ctg   1252
Arg Pro Ala Gly Thr Asp Gly Trp Ser Glu Glu Glu Leu Thr Lys Leu
        170                 175                 180

gtg agc cgg gac tcg atg atc ggt gtc agt aat gcg ctc aca ccg cag   1300
Val Ser Arg Asp Ser Met Ile Gly Val Ser Asn Ala Leu Thr Pro Gln
    185                 190                 195
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gaa gtg atc gta tga 1315
Glu Val Ile Val
200

<210> 105
<211> 29
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<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 105
ccggaattcg aaaggaatga ggaaatgga 29

<210> 106
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 106
aaaaagtact catacgatca cttcctgc 28

<210> 107
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 107
gttttcccag tcacgac 17

<210> 108
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 108
ggccagtgcc tagcttacat 20

<210> 109
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
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<400> 109
caggaaacag ctatgac 17

<210> 110
<211> 29
<212> DNA
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<223> a, c, g, t, unknown or other

<400> 110
gggcatatcg tggnnngaca agtcgcggt 29

<210> 111
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<222> (7)..(9)
<223> a, c, g, t, unknown or other

<400> 111
ctcaccnnnt cgatgatc 18

<210> 112
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<223> a, c, g, t, unknown or other

<400> 112
tacgagnnng aggtcggc 18

<210> 113
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<400> 113
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<210> 114
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<210> 115
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<223> a, c, g, t, unknown or other

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<210> 116
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<400> 116
aaggcgnnng cgtgagcg 18

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<223> a, c, g, t, unknown or other

<400> 117
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<210> 118
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<400> 118
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<400> 119
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<400> 120
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<210> 123
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<400> 123
ggcttcnnng gcctggac 18

<210> 124
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<400> 124
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<210> 125
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<400> 125
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<210> 126
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<400> 126
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<210> 127
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<400> 127
tggcacnnna tccgcacc 18

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<210> 132
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<400> 133
cgcgcgnnnt acgtgcgc 18

<210> 134
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<400> 134
accgggnnng tggtcaag 18

<210> 135
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<400> 135
gtggtcnnnc accacggc 18

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ggcgcgnnna tctacccg 18

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<400> 138
tactacnnnt gctgggag 18

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tacgacnnnt gggagccc 18

<210> 140
<211> 229
<212> PRT
<213> Rhodococcus rhodochrous

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Met	Asp	Gly	Ile	His	Asp	Thr	Gly	Gly	Met	Thr	Gly	Tyr	Gly	Pro	Val
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Pro	Tyr	Gln	Lys	Asp	Glu	Pro	Phe	Phe	His	Tyr	Glu	Trp	Glu	Gly	Arg
			20					25					30		

Thr	Leu	Ser	Ile	Leu	Thr	Trp	Met	His	Leu	Lys	Gly	Ile	Ser	Trp	Trp
		35					40					45			

Asp	Lys	Ser	Arg	Phe	Phe	Arg	Glu	Ser	Met	Gly	Asn	Glu	Asn	Tyr	Val
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Asn	Glu	Ile	Arg	Asn	Ser	Tyr	Tyr	Thr	His	Trp	Leu	Ser	Ala	Ala	Glu
65					70					75					80

Arg Ile Leu Val Ala Asp Lys Ile Ile Thr Glu Glu Glu Arg Lys His
85 90 95

Arg Val Gln Glu Ile Leu Glu Gly Arg Tyr Thr Asp Arg Lys Pro Ser
100 105 110

Arg Lys Phe Asp Pro Ala Gln Ile Glu Lys Ala Ile Glu Arg Leu His
115 120 125

Glu Pro His Ser Leu Ala Leu Pro Gly Ala Glu Pro Ser Phe Ser Leu
130 135 140

Gly Asp Lys Ile Lys Val Lys Ser Met Asn Pro Leu Gly His Thr Arg
145 150 155 160

Cys Pro Lys Tyr Val Arg Asn Lys Ile Gly Glu Ile Val Ala Tyr His
165 170 175

Gly Cys Gln Ile Tyr Pro Glu Ser Ser Ser Ala Gly Leu Gly Asp Asp
180 185 190

Pro Arg Pro Leu Tyr Thr Val Ala Phe Ser Ala Gln Glu Leu Trp Gly
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Asp Asp Gly Asn Gly Lys Asp Val Val Cys Val Asp Leu Trp Glu Pro
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Tyr Leu Ile Ser Ala
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Ala Ile Glu Thr Leu Leu Tyr Glu Arg Gly Leu Ile Thr Pro Ala Ala
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Val Asp Arg Val Val Ser Tyr Tyr Glu Asn Glu Ile Gly Pro Met Gly
35 40 45

Gly Ala Lys Val Val Ala Lys Ser Trp Val Asp Pro Glu Tyr Arg Lys
50 55 60

Trp Leu Glu Glu Asp Ala Thr Ala Ala Met Ala Ser Leu Gly Tyr Ala
65 70 75 80

Gly Glu Gln Ala His Gln Ile Ser Ala Val Phe Asn Asp Ser Gln Thr
85 90 95

His His Val Val Val Cys Thr Leu Cys Ser Cys Tyr Pro Trp Pro Val
100 105 110

Leu Gly Leu Pro Pro Ala Trp Tyr Lys Ser Met Glu Tyr Arg Ser Arg
115 120 125

Val Val Ala Asp Pro Arg Gly Val Leu Lys Arg Asp Phe Gly Phe Asp
130 135 140

Ile Pro Asp Glu Val Glu Val Arg Val Trp Asp Ser Ser Ser Glu Ile
145 150 155 160

Arg Tyr Ile Val Ile Pro Glu Arg Pro Ala Gly Thr Asp Gly Trp Ser
165 170 175

Glu Glu Glu Leu Thr Lys Leu Val Ser Arg Asp Ser Met Ile Gly Val
180 185 190

Ser Asn Ala Leu Thr Pro Gln Glu Val Ile Val
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